



#13

SEQUENCE LISTING

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Lys Phe ,Leu Leu Tyr Tyr Ala Gly Glu Val Ala Arg Lys Arg Lys Ala
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Glu Gly Leu Lys Leu Asn Gln Pro Glu Ala Ile Ala Tyr Ile Ser Ala
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His Ile Met Asp Glu Ala Arg Arg Gly Lys Lys Thr Val Ala Gln Leu
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Met Glu Glu Cys Met His Phe Leu Lys Lys Asp Glu Val Met Pro Gly
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Val Gly Asn Met Val Pro Asp Leu Gly Val Glu Ala Thr Phe Pro Asp
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Gly Thr Lys Leu Val Thr Val Asn Trp Pro Ile Glu Pro Asp Glu His
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Phe Lys Ala Gly Glu Val Lys Phe Gly Cys Asp Lys Asp Ile Glu Leu
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Asn Ala Gly Lys Glu Val Thr Glu Leu Glu Val Thr Asn Glu Gly Pro
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Lys Ser Leu His Val Gly Ser His Phe His Phe Phe Glu Ala Asn Lys
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Ala Leu Lys Phe Asp Arg Glu Lys Ala Tyr Gly Lys Arg Leu Asp Ile
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ccc tct ggc aac acg cta cgc att ggg gca gga caa acc cgc aaa gtg 760
 Pro Ser Gly Asn Thr Leu Arg Ile Gly Ala Gly Gln Thr Arg Lys Val
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 Gln Leu Ile Pro Leu Gly Gly Ser Lys Lys Val Ile Gly Met Asn Gly
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ctt gtg aat aac atc gcg gat gaa cgc cat aaa cat aaa gcg ctt gac 856
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gac att ggg att aaa aac ggc aaa atc cat ggc att ggc aag gca gga 1193
Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly Lys Ala Gly
315 320 325

aac aag gac atg caa gat⁷ ggc gta agc cct cat atg gtc gtg ggt gtg 1241
Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val Val Gly Val
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Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Thr Gly Pro Val
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Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp Asn Leu His
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Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly Thr Thr Pro
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agt gcg atc gat cac tgc ttg agc gtg gca gat gaa tac gat gtg caa 1625

Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr Asp Val Gln
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Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr Val Asp Asp
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Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr His Ile Glu
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600 605 610

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Lys Leu Pro Glu Asp Gly Lys Asp Asn Asp Asn Phe Arg Ile Lys Arg
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Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp Leu Val Val
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Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val Ile Lys Gly
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Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His His Lys
695 700 705 710

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Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val Ala Tyr Glu
715 720 725

aat ggc gtg aaa gaa aag ctg ggc tta gag cgc caa gtt cta ccg gtc 2441
Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Gln Val Leu Pro Val
730 735 740

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Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe Asn Asp Lys
745 750 755

acg gca aaa atc acc gtc gat ccg aaa acc ttc gag gtc ttt gta gat 2537

Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val Phe Val Asp
760 765 770

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775 780 785 790

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Arg Tyr Thr Phe Phe
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Arg Gly Lys Lys Thr Val Ala Gln Leu Met Glu Glu Cys Met His Phe

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Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
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Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
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Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
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35 40 45

Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
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Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95

Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
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Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140

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180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
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Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
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Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
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Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270

His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met
275 280 285

Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
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His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Met
340 345 350

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Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
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Glu Phe Gly Lys Leu Pro Glu Asp Gly Lys Asp Asn Asp Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
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Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
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Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
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485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Gln Val
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Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
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Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val
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Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
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ccc gaa gcc att gcc tac att agt gcc cat att atg gac gag gcg cgc 144
Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45

cgt ggc aaa aaa acc gtt gct gaa ctt atg gaa gaa tgt atg cac ttt 192
Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

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Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

ttg ggc gta gaa gcc act ttc ccc gat ggc acc aaa ctc gta acc gtg 288
Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

aat tgg ccc att gaa cct gat gaa cac ttt aaa gcc ggt gaa gtg aaa 336
Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

ttt ggc tgt gat aaa gac att gag ctc aac gcg ggt aag gaa gtt acc 384
Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125

gag ctt gaa gtt acc aac gaa gga cct aaa tcc ttg cat gtg ggt agc 432
Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

cat ttc cac ttc ttt gaa acc aac aag gca ttg aaa ttc gat cgg gaa 480
His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu
145 150 155 160

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Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

att ggg gca gga caa acc cgt aaa gtg cag tta atc cct ctt ggc ggt 576
Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

agt aaa aaa gtg att ggc atg aac ggg ctt gtg aat aat att gcg gac 624
Ser Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

gaa cgc cat aaa cac aaa gca cta gac aag gca aaa tct cac gga ttc 672
Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
210 215 220

atc aag taa ggagactccc atg aaa atg aaa aaa caa gag tat gta aac 721
Ile Lys Met Lys Met Lys Lys Gln Glu Tyr Val Asn
225 230 235

acc tac gga ccc acc aca ggc gat aaa gtg cgc tta gga gat acc gat 769
Thr Tyr Gly Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr Asp

240 245 250
ctt tgg gca gaa gta gaa cat gac tat acc act tat ggc gaa gag ctc 817
Leu Trp Ala Glu Val Glu His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu
255 260 265

aaa ttt ggc gcg ggt aaa act atc cgt gag ggt atg ggt cag agc aat 865
Lys Phe Gly Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser Asn
270 275 280 285

agc cca gat gaa aac acc tta gat tta gtg atc acc aac gcg atg att 913
Ser Pro Asp Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met Ile
290 295 300

atc gac tac acc ggg att tat aaa gcc gac att ggt att aaa aat ggc 961
Ile Asp Tyr Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly
305 310 315

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Lys Ile His Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly
320 325 330

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335 340 345

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Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His Phe
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370 375 380

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Met Phe Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr Thr
385 390 395

atc act ccg ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gct gaa 1249
Ile Thr Pro Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala Glu
400 405 410

gag tat tct atg aat gtg ggc ttt ttg ggc aaa ggc aat agc tcc agt 1297
Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser
415 420 425

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430 435 440 445

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Leu His Glu Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys Leu
450 455 460

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Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp Thr
465 470 475

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Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn Gly
480 485 490

cgc gcc atc cat gcc tac cac att gag gga gcg ggc gga gga cac tca 1537
Arg Ala Ile His Ala Tyr His Ile Glu Gly Ala Gly Gly His Ser
495 500 505

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Pro Asp Val Ile Thr Met Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser
510 515 520 525

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Thr Thr Pro Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His Leu
530 535 540

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Asp Met Leu Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu Asp

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560	565	570	
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575	580	585	
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590	595	600	605
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655	660	665	
gta aaa ccc aaa atc gtg atc aaa ggc ggt atg gtg gtg ttc tct gaa Val Lys Pro Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser Glu			2065
670	675	680	685
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Arg Glu Met Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile
705 710 715

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Thr Phe Val Ser Lys Val Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu
720 725 730

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735 740 745

aag aaa gac ttc aaa ttc aac aac aag acg gcg cat atc act gtc gat 2305
Lys Lys Asp Phe Lys Phe Asn Asn Lys Thr Ala His Ile Thr Val Asp
750 755 760 765

cct aaa acc ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa 2353
Pro Lys Thr Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys
770 775 780

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35 40 45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu
145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
210 215 220

Ile Lys

<210> 6

<211> 568

<212> PRT

<213> Helicobacter felis

<400> 6

Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Thr
1 5 10 15

Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu
20 25 30

His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
35 40 45

Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80

Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95

Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
100 105 110

Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
115 120 125

Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140

Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Thr
145 150 155 160

Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
165 170 175

Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
195 200 205

Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220

Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270

His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met
275 280 285

Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala

355

360

365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
500 505 510

Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
515 520 525

Asn Asn Lys Thr Ala His Ile Thr Val Asp Pro Lys Thr Phe Glu Val
530 535 540

Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Ala Ser Glu Val Pro
545 550 555 560

Leu Ala Gln Arg Tyr Thr Phe Phe

565

<210> 7

<211> 2183

<212> DNA

<213> Helicobacter felis

<220>

<221> CDS

<222> (3)...(683)

<220>

<221> CDS

<222> (694)...(2181)

<400> 7

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Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr

1

5

10

15

gcg ggc gaa gtg gct aga aag cgc aaa gca gag ggc tta aag ctc aat 95

Ala Gly Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn

20

25

30

caa ccc gaa gcc att gcc tac att agt gcc cat att atg gac gag gcg 143

Gln Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala

35

40

45

cgc cgt ggc aaa aaa acc gtt gct gaa ctt atg gaa gaa tgt atg cac 191

Arg Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His

50

55

60

ttt ttg aaa aaa gat gag gtg atg ccc ggt gtg ggg aat atg gtc cct 239

Phe Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro

65

70

75

gat ttg ggc gta gaa gcc act ttc ccc gat ggc acc aaa ctc gta acc 287
 Asp Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr
 80 85 90 95

gtg aat tgg ccc att gaa cct gat gaa cac ttt aaa gcc ggt gaa gtg 335
 Val Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val
 100 105 110

aaa ttt ggc tgt gat aaa gac att gag ctc aac gtg ggt aag gaa gtt 383
 Lys Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Val Gly Lys Glu Val
 115 120 125

acc gag ctt gaa gtt acc aac gaa gga cct aaa tcc ttg cat gtg ggt 431
 Thr Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly
 130 135 140

agc cat ttc cac ttc ttt gaa acc aac aag gca ttg aaa ttc gat cgg 479
 Ser His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg
 145 150 155

gaa aaa gcc tat ggc aaa cgc cta gat att ccc tct ggc aac acg cta 527
 Glu Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu
 160 165 170 175

cgc att ggg gca gga caa acc cgt aaa gtg cag tta atc cct ctt ggc 575
 Arg Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly
 180 185 190

ggt agt aaa aaa gtg att ggc atg aac ggg ctt gtg aat aat att gcg 623
 Gly Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala
 195 200 205

gac gaa cgc cat aaa cac aaa gca cta gac aag gca aaa tct cac gga 671
 Asp Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly
 210 215 220

ttc atc aag taa ggagactccc atg aaa atg aaa caa gag tat gta 720

Phe Ile Lys	Met Lys Met Lys Lys Gln Glu Tyr Val	
225	230	235
aac acc tac gga ccc acc aca ggc gat aaa gtg cgc tta gga gat acc		768
Asn Thr Tyr Gly Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr		
240	245	250
gat ctt tgg gca gaa gta gaa cat gac tat acc act tat ggc gaa gag		816
Asp Leu Trp Ala Glu Val Glu His Asp Tyr Thr Thr Tyr Gly Glu Glu		
255	260	265
ctc aaa ttt ggc gcg ggt aaa act atc cgt gag ggt atg ggt cag agc		864
Leu Lys Phe Gly Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser		
270	275	280
aat agc cca gat gaa aac acc tta gat tta gtg atc acc aac gcg atg		912
Asn Ser Pro Asp Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met		
285	290	295
att atc gac tac acc ggg att tat aaa gcc gac att ggt att aaa aat		960
Ile Ile Asp Tyr Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn		
305	310	315
ggc aaa atc cat ggt att ggc aag gcg ggg aac aaa gac atg caa gat		1008
Gly Lys Ile His Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp		
320	325	330
ggc gta agc cct cat atg gtc gtg ggt gtg ggc aca gaa gca cta gca		1056
Gly Val Ser Pro His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala		
335	340	345
ggg gaa ggt atg att att acc gct ggg ggg atc gat tcg cac acc cac		1104
Gly Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His		
350	355	360
ttc ctc tct ccc caa caa ttc cct acc gct cta gcc aat ggt gtt aca		1152
Phe Leu Ser Pro Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr		
365	370	375
		380

acc atg ttt gga ggt ggc aca ggt ccg gta gat ggc acg aat gcg acc 1200
Thr Met Phe Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr
385 390 395

acc atc act ccg ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gct 1248
Thr Ile Thr Pro Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala
400 405 410

gaa gag tat tct atg aat gta ggc ttt ttg ggc aaa ggc aat agt tct 1296
Glu Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser
415 420 425

agc aaa aaa caa ctt gta gaa caa gta gaa gcg ggc gcg att ggc ttt 1344
Ser Lys Lys Gln Leu Val Glu Gln Val Glu Ala Gly Ala Ile Gly Phe
430 435 440

aaa ttg cat gaa gac tgg ggc aca aca cca agt gcg atc gat cac tgc 1392
Lys Leu His Glu Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys
445 450 455 460

ttg agc gtg gca gat gaa tac gat gtg caa gtt tgt atc cac acc gat 1440
Leu Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp
465 470 475

acg gtc aat gag gca ggt tat gtg gat gac acc cta aat gca atg aac 1488
Thr Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn
480 485 490

ggg cgc gcc atc cat gcc tac cac att gag gga gcg ggc gga gga cac 1536
Gly Arg Ala Ile His Ala Tyr His Ile Glu Gly Ala Gly Gly His
495 500 505

tca cct gat gtt atc acc atg gca ggc gag ctc aat att cta ccc tcc 1584
Ser Pro Asp Val Ile Thr Met Ala Gly Glu Leu Asn Ile Leu Pro Ser
510 515 520

tcc acc acc ccc act att ccc tat acc att aat acg gtt gca gaa cac 1632

Ser Thr Thr Pro Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His
525 530 535 540

tta gac atg ctc atg acc tgc cac cac cta gat aag cgc atc cgc gag 1680
Leu Asp Met Leu Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu
545 550 555

gat tta caa ttt tct caa agc cgt atc cgc ccc gga tct att gcc gct 1728
Asp Leu Gln Phe Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala
560 565 570

gag gat gtg ctc cat gat att ggc gtg atc gcg atg act agc tcc gat 1776
Glu Asp Val Leu His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp
575 580 585

tcg caa gca atg ggg cgc gct ggg gaa gtg att cct aga act tgg caa 1824
Ser Gln Ala Met Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln
590 595 600

act gca gat aag aat aaa aaa gaa ttt ggt aag ctt cct gaa gat ggt 1872
Thr Ala Asp Lys Asn Lys Lys Glu Phe Gly Lys Leu Pro Glu Asp Gly
605 610 615 620

gca gat aac gac aac ttc cgc atc aaa cgc tat atc tcc aaa tac acc 1920
Ala Asp Asn Asp Asn Phe Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr
625 630 635

att aat ccc gct ttg acc cat ggc gtg agc gag tat atc ggc tct gtg 1968
Ile Asn Pro Ala Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val
640 645 650

gaa gag ggc aag atc gcc gac ttg gtg gtg tgg aat cct gcc ttt ttt 2016
Glu Glu Gly Lys Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe
655 660 665

ggc gtg aaa cct aag att gtg att aaa ggt ggc atg gtg gtc ttc tct 2064
Gly Val Lys Pro Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser
670 675 680

gaa atg ggc gat tct aac gcg tcc gtg ccc acg cct cag ccg gtt tat 2112
Glu Met Gly Asp Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr
685 690 695 700

tac cgc gaa atg ttt ggg cac cac ggc aag gcg aaa ttt gac acc agc 2160
Tyr Arg Glu Met Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser
705 710 715

atc act ttt cgt gtc tca agc gg 2183
Ile Thr Phe Arg Val Ser Ser
720

<210> 8
<211> 226
<212> PRT
<213> Helicobacter felis

<400> 8
Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
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Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Val Gly Lys Glu Val Thr
115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

His Phe His Phe Phe Glu Thr Asn Lys Ala Leu Lys Phe Asp Arg Glu
145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
210 215 220

Ile Lys
225

<210> 9
<211> 496
<212> PRT
<213> Helicobacter felis

<400> 9
Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Thr
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Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu

20 25 30

His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
35 40 45

Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80

Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95

Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
100 105 110

Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
115 120 125

Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140

Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Thr
145 150 155 160

Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
165 170 175

Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
195 200 205

Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220

Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270

His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met
275 280 285

Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Arg Val Ser Ser
485 490 495

<210> 10

<211> 2407

<212> DNA

<213> Helicobacter felis

<220>

<221> CDS

<222> (2)..(682)

<220>

<221> CDS

<222> (693)..(2399)

<400> 10

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Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala

1

5

10

15

ggc gaa gtg gct aga aag cgc aaa gcg gag ggc tta aag ctc aac caa 97
Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30

ccc gaa gcc att gcc tac att agt gcc cat att atg gac gag gcg cgc 145

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45

cgt ggc aaa aag acc gtt gcg gaa ctt atg gaa gag tgt atg cac ttt 193
Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

ttg aaa aaa gac gag gtg atg ccc ggt gtg ggg aat atg gtc cct gat 241
Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

tta ggc gtg gaa gct act ttt ccc gat ggc acc aaa ctc gta acc gtg 289
Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

aat tgg ccc atc gaa ccc gat gaa cac ttc aaa gcg ggc gaa gtc aaa 337
Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

ttt ggc tgt gat aaa gac att gaa ctc aac gca ggt aag gaa gtt acc 385
Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125

gaa cta gaa gtt acc aac gaa gga cct aaa tcc ttg cat gtg ggt agc 433
Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

cat ttc cac ttc ttt gaa gcc aac aag gca ttg aaa ttc gat cgg gaa 481
His Phe His Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
145 150 155 160

aaa gcc tat ggc aaa cgc cta gat att ccc tct ggc aac acg cta cgc 529
Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

att ggg gca gga caa acc cgt aaa gtg cag tta atc cct ctt ggc ggc 577
Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

agt aaa aaa gtg att ggc atg aac ggg ctt gtg aat aat att gca gat 625
Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

gaa cgc cat aaa cac aaa gcg tta gaa aaa gca aaa tct cac gga ttt 673
Glu Arg His Lys His Lys Ala Leu Glu Lys Ala Lys Ser His Gly Phe
210 215 220

atc aaa taa ggagactccc atg aaa atg aaa aaa caa gag tat gta aat 722
Ile Lys Met Lys Met Lys Gln Glu Tyr Val Asn
225 230 235

acc tac gga cct acc aca ggc gac aaa gtg cgc tta gga gat acc gat 770
Thr Tyr Gly Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr Asp
240 245 250

ctt tgg gca gaa gta gaa cat gac tat acc act tat ggc gaa gag ctc 818
Leu Trp Ala Glu Val Glu His Asp Tyr Thr Tyr Gly Glu Glu Leu
255 260 265

aaa ttt ggc gcg ggt aaa act atc cgt gag ggc atg ggt cag agc aat 866
Lys Phe Gly Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser Asn
270 275 280 285

agt cca gat gaa aac acc cta gat tta gtc atc acc aac gcg atg att 914
Ser Pro Asp Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met Ile
290 295 300

att gac tac acc ggg att tac aaa gcc gac att ggc att aaa aat ggc 962
Ile Asp Tyr Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly
305 310 315

aaa atc cat ggc att ggc aag gca gga aac aag gac atg caa gat ggc 1010
Lys Ile His Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly
320 325 330

gta agc cct cat atg gtc gtg ggt gtg ggc aca gaa gca tta gca ggg 1058

Val Ser Pro His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala Gly
335 340 345

gaa ggt atg att att acc gct ggg ggg atc gat tca cac acc cac ttc 1106
Glu Gly Met Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His Phe
350 355 360 365

ctc tct cca caa caa ttc cct acc gct cta gcc aat ggc gtt aca acc 1154
Leu Ser Pro Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr Thr
370 375 380

atg ttt ggc ggt ggc aca ggt ccg gta gat ggc acg aat gcg act acc 1202
Met Phe Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr Thr
385 390 395

atc act ccg ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gct gaa 1250
Ile Thr Pro Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala Glu
400 405 410

gag tat tct atg aat gtg ggc ttt ttg ggc aaa ggc aat agc tcc agt 1298
Glu Tyr Ser Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser
415 420 425

aaa aaa caa ctt gta gaa caa ata gaa gcg ggc gcg atc ggc ttt aaa 1346
Lys Lys Gln Leu Val Glu Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys
430 435 440 445

ttg cat gaa gac tgg ggc aca act cca agt gca atc gat cac tgc ttg 1394
Leu His Glu Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys Leu
450 455 460

agc gta gca gat gaa tac gat gtg caa gtt tgt atc cac acc gat acg 1442
Ser Val Ala Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp Thr
465 470 475

gtc aat gag gca ggt tat gta gat gac acc ctg aat gcg atg aac ggg 1490
Val Asn Glu Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn Gly
480 485 490

cgc gcc atc cat gcc tac cac att gag gga gcg ggc gga gga cac tca 1538
 Arg Ala Ile His Ala Tyr His Ile Glu Gly Ala Gly Gly His Ser
 495 500 505

cct gat gtt atc acc atg⁷ gca ggc gag ctc aat att cta ccc tcc tcc 1586
 Pro Asp Val Ile Thr Met Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser
 510 515 520 525

aca acc ccc act atc ccc tat acc att aat acg gtt gca gaa cac tta 1634
 Thr Thr Pro Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His Leu
 530 535 540

gac atg ctc atg acc tgc cac cac cta gat aaa cgc atc cgc gag gat 1682
 Asp Met Leu Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu Asp
 545 550 555

tta caa ttt tcc caa agc cgt atc cgc ccc ggc tct atc gcc gct gaa 1730
 Leu Gln Phe Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu
 560 565 570

gat gtg ctc cat gat att ggc gtg atc gcg atg aca agc tcg gat tcg 1778
 Asp Val Leu His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp Ser
 575 580 585

caa gca atg ggg cgc gct ggc gaa gtg att cct cga act tgg cag act 1826
 Gln Ala Met Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln Thr
 590 595 600 605

gcg gat aag aat aaa aaa gaa ttt ggt aag ctt cct gaa gat agt gca 1874
 Ala Asp Lys Asn Lys Lys Glu Phe Gly Lys Leu Pro Glu Asp Ser Ala
 610 615 620

gat aac gac aac ttc cgt atc aaa cgc tac atc tcc aaa tac act att 1922
 Asp Asn Asp Asn Phe Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile
 625 630 635

aac ccc gct cta acc cat ggg gta agc gag tat atc ggc tct gtg gaa 1970

Asn Pro Ala Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val Glu
640 645 650

gag ggc aaa atc gct gat ttg gtg tgg aat cct gcc ttt ttt ggt 2018
Glu Gly Lys Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe Gly
655 660 665

gtg aaa cct aag att gtg atc aaa ggc ggt atg gtg gtc ttc tct gaa 2066
Val Lys Pro Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser Glu
670 675 680 685

atg ggc gac tcc aac gcg tcc gtg cct aca cct cag ccg gtt tat tac 2114
Met Gly Asp Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr
690 695 700

cgc gaa atg ttt ggg cat cac ggc aag gcg aaa ttt gac acc agc atc 2162
Arg Glu Met Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile
705 710 715

act ttt gtt tcc aaa gtc gcc tat gaa aat ggc gtg aaa gaa aaa cta 2210
Thr Phe Val Ser Lys Val Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu
720 725 730

ggc tta gag cgc aag gtg cta ccc gtg aaa aac tgc cgc aac atc act 2258
Gly Leu Glu Arg Lys Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr
735 740 745

aag aaa gac ttc aaa ttc aac aac aag acg gcg cat atc act gtc gat 2306
Lys Lys Asp Phe Lys Phe Asn Asn Lys Thr Ala His Ile Thr Val Asp
750 755 760 765

cct aaa acc ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa 2354
Pro Lys Thr Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys
770 775 780

ccc gcc tct gaa gtg cct cta gcc cag cgc tac act ttc ttc tag 2399
Pro Ala Ser Glu Val Pro Leu Ala Gln Arg Tyr Thr Phe Phe
785 790 795

gcncaatg

2407

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<212> PRT
<213> Helicobacter felis

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Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu

145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

Glu Arg His Lys His Lys Ala Leu Glu Lys Ala Lys Ser His Gly Phe
210 215 220

Ile Lys

225

<210> 12

<211> 568

<212> PRT

<213> Helicobacter felis

<400> 12

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20 25 30

His Asp Tyr Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys
35 40 45

Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80

Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95

Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
100 105 110

Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
115 120 125

Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140

Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Thr
145 150 155 160

Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
165 170 175

Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
195 200 205

Gln Ile Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220

Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270

His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met

275 280 285
Ala Gly Glu Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Ser Ala Asp Asn Asp Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
450 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
500 505 510

Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
515 520 525

Asn Asn Lys Thr Ala His Ile Thr Val Asp Pro Lys Thr Phe Glu Val
530 535 540

Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Ala Ser Glu Val Pro
545 550 555 560

Leu Ala Gln Arg Tyr Thr Phe Phe
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<210> 13

<211> 2452

<212> DNA

<213> Helicobacter felis

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<221> CDS

<222> (48)..(728)

<220>

<221> CDS

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<400> 13

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Val Lys Leu

aca ccc aaa gag caa gaa aag ttc ttg tta tat tat gcg ggc gaa gtg 104
Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala Gly Glu Val
5 10 15

gct aga aag cgc aaa gca gag ggc tta aag ctc aac caa ccc gaa gcc 152
Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln Pro Glu Ala
20 25 30 35

att gcc tac att agt gcc cat att atg gac gag gcg cgt cgt ggc aaa 200
Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg Arg Gly Lys
40 45 50

aaa acc gtt gcg gaa ctt atg gaa gag tgt atg cac ttt ttg aaa aaa 248
Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe Leu Lys Lys
55 60 65

gac gag gtg atg ccc ggg gtg ggg aat atg gtc cct gat ttg ggc gtg 296
Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp Leu Gly Val
70 75 80

gaa gcc act ttc ccc gat ggc acc aaa ctc gta act gtg aat tgg ccc 344
Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val Asn Trp Pro
85 90 95

atc gaa cct gat gaa cac ttt aag gcg ggt gaa gtg aaa ttt ggc tgt 392
Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys Phe Gly Cys
100 105 110 115

gat aaa gac att gaa ctc aac gca ggt aag gaa gtt acc gaa cta gaa 440
Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr Glu Leu Glu
120 125 130

gtt act aac gaa gga cct aaa tcc ttg cat gtg ggt agc cat ttc cac 488
Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser His Phe His
135 140 145

ttc ttt gaa gcc aac aaa gca ttg aaa ttc gat cgg gaa aaa gcc tat 536
Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu Lys Ala Tyr

150 155 160
ggc aaa cgc cta gat att ccc tct ggc aac aca cta cgc att ggg gca 584
Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg Ile Gly Ala
165 170 175
gga caa acc cgt aaa gtg cag tta atc cct ctt ggc ggt agt aaa aaa 632
Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly Ser Lys Lys
180 185 190 195
gtg att ggc atg aac ggg ctt gtg aat aat att gcg gac gaa cgc cat 680
Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp Glu Arg His
200 205 210
aaa cac aaa gcg cta gac aaa gca aaa tct cac gga ttt atc aag taa 728
Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe Ile Lys
215 220 225
ggagactccc atg aaa atg aaa aaa caa gag tat gta aat acc tac gga 777
Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly
230 235 240
ccc acc aca ggc gat aaa gtg cgc tta gga gat acc gat ctt tgg gca 825
Pro Thr Thr Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala
245 250 255
gaa gta gaa cat gac tat acc acc tat ggc gaa gaa ctc aaa ttc ggt 873
Glu Val Glu His Asp Tyr Thr Tyr Gly Glu Glu Leu Lys Phe Gly
260 265 270
gca ggt aaa act atc cgt gag ggt atg ggt cag agc aat agc cca gat 921
Ala Gly Lys Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp
275 280 285
gaa aac acc tta gat tta gtg atc acc aac gcg atg att att gac tac 969
Glu Asn Thr Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr
290 295 300

acc ggg att tac aaa gcc gac att ggc att aaa aat ggc aaa atc cat 1017
Thr Gly Ile Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His
305 310 315 320

ggc att ggc aag gca gga aac aag gac atg caa gat ggc gta agc cct 1065
Gly Ile Gly Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro
325 330 335

cat atg gtc gtg ggt gtg ggc aca gaa gca cta gca ggg gaa ggt atg 1113
His Met Val Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met
340 345 350

att att acc gct ggg ggg atc gat tca cac acc cac ttc ctc tct cca 1161
Ile Ile Thr Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro
355 360 365

caa caa ttc cct acc gct cta gcc aat ggc gtt aca aca atg ttt ggc 1209
Gln Gln Phe Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly
370 375 380

ggc aca ggc ccc gta gat ggc acg aat gcg act acc atc act ccg 1257
Gly Gly Thr Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro
385 390 395 400

ggc aaa tgg aac ttg cac cgc atg ttg cgc gca gca gaa gag tat tct 1305
Gly Lys Trp Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser
405 410 415

atg aat gtg ggc ttt ttg ggc aaa ggc aat agc tct agt aaa aaa caa 1353
Met Asn Val Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln
420 425 430

ctt gta gaa caa gta gaa gcg ggc gcg att ggt ttt aaa ttg cat gaa 1401
Leu Val Glu Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu
435 440 445

gac tgg ggc aca act cca agt gcg atc gat cac tgc ttg agc gta gca 1449
Asp Trp Gly Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala

450	455	460	
gat gaa tac gat gtg caa gtt tgt ata cac acc gat acg gtc aat gag			1497
Asp Glu Tyr Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu			
465	470	475	480
<i>#</i>			
gca ggt tat gta gat gac acc cta aat gca atg aac ggg cgc gcc atc			1545
Ala Gly Tyr Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile			
485	490	495	
cat gcc tac cac att gag gga gcg ggt gga gga cac tca cct gat gtt			1593
His Ala Tyr His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val			
500	505	510	
atc acc atg gca ggc gaa gtg aat att cta ccc tcc tcc aca acc cct			1641
Ile Thr Met Ala Gly Glu Val Asn Ile Leu Pro Ser Ser Thr Thr Pro			
515	520	525	
act atc ccc tat acc att aat acg gtt gca gaa cac tta gac atg ctt			1689
Thr Ile Pro Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu			
530	535	540	
atg acc tgc cac cac cta gat aaa cgc atc cgc gag gat ctccaa ttt			1737
Met Thr Cys His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe			
545	550	555	560
tct caa agc cgt atc cgc ccc ggc tct atc gcc gct gaa gat gtg ctc			1785
Ser Gln Ser Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu			
565	570	575	
cat gat atc ggt gtg atc gcg atg aca agt tcc gat tcg caa gca atg			1833
His Asp Ile Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met			
580	585	590	
ggg cgc gct ggg gaa gtg att cct aga act tgg caa act gca gac aag			1881
Gly Arg Ala Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys			
595	600	605	

aat aaa aaa gaa ttt ggt aag ctt cct gaa gat ggt gca gat aat gac 1929
Asn Lys Lys Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asp
610 . 615 620

aac ttc cgc atc aaa cgc tat atc tcc aaa tac acc att aat ccc gct 1977
Asn Phe Arg Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala
625 630 635 640

ttg acc cat ggc gtg agc gag tat atc ggc tct gtg gaa gag ggc aag 2025
Leu Thr His Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys
645 650 655

atc gcc gac ttg gtg gtg tgg aat cct gcc ttt ttt ggc gta aaa ccc 2073
Ile Ala Asp Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro
660 665 670

aaa atc gtg atc aaa ggc ggt atg gtg gtg ttc tct gaa atg ggc gat 2121
Lys Ile Val Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp
675 680 685

tct aat gcg tct gtg ccc act cct cag ccg gtt tat tac cgc gaa atg 2169
Ser Asn Ala Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met
690 695 700

ttt ggg cat cac ggc aag gcg aaa ttt gac acc agc atc act ttt gtt 2217
Phe Gly His His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val
705 710 715 720

tcc aaa gtc gcc tat gaa aat ggt gtg aaa gaa aaa cta ggt tta gag 2265
Ser Lys Val Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu
725 730 735

cgc aag gtg ctc ccc gtg aaa aac tgc cgt aac atc acc aag aag gac 2313
Arg Lys Val Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp
740 745 750

ttc aag ttc aac gac aaa act gca aaa atc acc gtc gat ccg aaa acc 2361
Phe Lys Phe Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr

755

760

765

ttc gag gtc ttt gta gat ggc aaa ctc tgc acc tct aaa ccc acc tct 2409
Phe Glu Val Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser

770

775

780

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gaa gtg cct cta gcc caa cgc tac act ttc ttc tag gcataat 2452
Glu Val Pro Leu Ala Gln Arg Tyr Thr Phe Phe

785

790

795

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<211> 226

<212> PRT

<213> Helicobacter felis

<400> 14

Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
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Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
20 25 30

Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
35 40 45

Arg Gly Lys Lys Thr Val Ala Glu Leu Met Glu Glu Cys Met His Phe
50 55 60

Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
65 70 75 80

Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
85 90 95

Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
100 105 110

Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
115 120 125

Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
130 135 140

His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
145 150 155 160

Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
165 170 175

Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
180 185 190

Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
195 200 205

Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
210 215 220

Ile Lys

225

<210> 15

<211> 568

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<213> Helicobacter felis

<400> 15

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20 25 30

His Asp Tyr Thr Thr Tyr Gly Glu Leu Lys Phe Gly Ala Gly Lys

35

40

45

Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
50 55 60

Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
65 70 75 80

Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
85 90 95

Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
100 105 110

Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
115 120 125

Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
130 135 140

Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Thr
145 150 155 160

Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp
165 170 175

Asn Leu His Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val
180 185 190

Gly Phe Leu Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu
195 200 205

Gln Val Glu Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly
210 215 220

Thr Thr Pro Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr
225 230 235 240

Asp Val Gln Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr
245 250 255

Val Asp Asp Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr
260 265 270

His Ile Glu Gly Ala Gly Gly His Ser Pro Asp Val Ile Thr Met
275 280 285

Ala Gly Glu Val Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro
290 295 300

Tyr Thr Ile Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys
305 310 315 320

His His Leu Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser
325 330 335

Arg Ile Arg Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Ile
340 345 350

Gly Val Ile Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala
355 360 365

Gly Glu Val Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys
370 375 380

Glu Phe Gly Lys Leu Pro Glu Asp Gly Ala Asp Asn Asn Phe Arg
385 390 395 400

Ile Lys Arg Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His
405 410 415

Gly Val Ser Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp
420 425 430

Leu Val Val Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val
435 440 445

Ile Lys Gly Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala
450 , 455 460

Ser Val Pro Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His
465 470 475 480

His Gly Lys Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val
485 490 495

Ala Tyr Glu Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Lys Val
500 505 510

Leu Pro Val Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe
515 520 525

Asn Asp Lys Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val
530 535 540

Phe Val Asp Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser Glu Val Pro
545 550 555 560

Leu Ala Gln Arg Tyr Thr Phe Phe
565

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<211> 21
<212> DNA
<213> Helicobacter felis

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catgcactt ttgaaaaag a 21

<210> 17
<211> 16

<212> DNA
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<400> 17
tatggtgttgc ttctct 16

<210> 18
<211> 32
<212> DNA
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<400> 18
ggagtaacat atgaaaactca cacccaaaga gc 32

<210> 19
<211> 27
<212> DNA
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<400> 19
cacaccacacg accatgtgag ggcttac 27

<210> 20
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<212> DNA
<213> Helicobacter felis

<400> 20
gtaagccctc acatggtcgt gggtg 27

<210> 21
<211> 34
<212> DNA
<213> Helicobacter felis

<400> 21

cgaattcgg a tcctagaaga aagtgttagcg ctgg

34